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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 11:29:08 ; Search time 41 Seconds  
(without alignments)

484.445 Million cell updates/sec

Title: US-10-018-878-9

Perfect score: 45

Sequence: 1 agccaaatttaaacagcgtag.....acatattgataatcagggttc 45

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:  
 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:  
 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:  
 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:  
 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:  
 5: /cgn2\_6/ptodata/2/ina/PC10S\_COMB.seq:  
 6: /cgn2\_6/ptodata/2/ina/backfiles.seq:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23.6	52.4	2453	4 US-08-961-527-316	Sequence 316, App
c	21.6	48.0	723	4 US-09-328-352-3411	Sequence 3411, App
c	21.2	47.1	580073	4 US-08-545-528D-1	Sequence 1, App
c	21	46.7	190	3 US-09-061-410-8	Sequence 8, App
c	21	46.7	190	4 US-09-722-458-8	Sequence 1040, AP
c	21	46.7	614	4 US-09-221-017B-1040	Sequence 599, App
c	21	46.7	786	4 US-09-328-352-599	Sequence 1397, AP
c	21	46.7	1521	4 US-09-328-352-1397	Sequence 6, App
c	21	46.7	2643	4 US-09-486-072-6	Sequence 72, App
c	21	46.7	46819	4 US-09-454-72	Sequence 1, App
c	20.8	46.2	1664976	4 US-08-916-421B-1	Sequence 1, App
c	20.8	46.2	1830121	4 US-09-577-884-1	Sequence 1, App
c	20.8	46.2	1830121	4 US-09-913-990A-1	Sequence 1, App
c	20.6	45.8	882	4 US-09-107-532A-1988	Sequence 1988, AP
c	20.6	45.8	1696	3 US-09-029-366-1	Sequence 1, App
c	20.4	45.3	1664976	4 US-08-916-421B-1	Sequence 1, App
c	20.2	44.9	1647	6 5405943-3	Patent No. 5405943
c	20	44.4	634	3 US-08-998-416-152	Sequence 152, App
c	19	44.4	2091	4 US-09-13-001C-1459	Sequence 1459, AP
c	20	44.4	3652	4 US-08-961-527-251	Sequence 251, App
c	19.8	44.0	2307	3 US-08-942-008-1	Sequence 1, App
c	19.8	44.0	2853	4 US-09-328-352-542	Sequence 542, App
c	19.8	44.0	7411	4 US-09-638-238-27	Sequence 27, App
c	19.8	44.0	7411	4 US-09-638-238-27	Sequence 27, App
c	19.8	44.0	148567	4 US-09-801-876B-3	Sequence 3, App
c	19.6	43.6	595	3 US-09-271-531-63	Sequence 63, App
c	19.6	43.6	846	4 US-08-936-165A-65	Sequence 65, App
c	19.6	43.6	1299	4 US-09-222-938A-38	Sequence 38, App

ALIGNMENTS

RESULT 1  
US-08-961-527-316  
; Sequence 316, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MS DOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brooks, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 316:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2453 base pairs  
; TYPE: nucleic acid  
; STRANDBODNESS: double  
; TOPOLOGY: linear  
; US-08-961-527-316

Query Match Local Similarity Score 23.6%; DB 4; Length 2453;  
Best Local Similarity 76.3%; Pred. No. 5.4;  
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 3 CAAACATTAACAGCGTGCATTACATATTGATAATCA 40  
Db 1335 CAAACATTAACAGCGTGCATTACATATTGATAATCA 1372

RESULT 2  
US-09-328-352-3411/c  
Sequence 3411, Application US/09328352  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GRP99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 3411  
LENGTH: 723  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-3411

Query Match Score 21.6; DB 4; Length 723;  
Best Local Similarity 68.2%; Pred. No. 25;  
Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 2 GCAACATTAACAGCGTGCATTACATATTGATAATCAGGTTTC 45  
Db 554 GCTAAATTAAAAGCTTAAGCTTAAGGTGGATAAGCGATAATCGGTTTC 511

RESULT 3  
US-08-545-528D-1  
Sequence 1, Application US/08545528D  
GENERAL INFORMATION:  
APPLICANT: Fraser et al.  
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment  
Patent No 6537773  
TITLE OF INVENTION: Thereof, and Uses Thereof  
FILE REFERENCE: PBL93P1  
CURRENT APPLICATION NUMBER: US/08/545,528D  
CURRENT FILING DATE: 1995-10-19  
PRIOR APPLICATION NUMBER: US 08/488,018  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/473,545  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 1  
SEQ ID NO 1  
LENGTH: 580073  
TYPE: DNA  
ORGANISM: Mycoplasma genitalium  
US-08-545-528D-1

Query Match Score 21.2%; DB 4; Length 580073;  
Best Local Similarity 69.0%; Pred. No. 63;  
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 4 AACATTAACAGCGTGCATTACATATTGATAATCAGGTTTC 45  
Db 67183 AACATTAACATTAACGTGGTTTATTATGATACTCACCTTC 67224

RESULT 4  
US-09-060-410-8  
Sequence 8, Application US/0960410  
GENERAL INFORMATION:  
APPLICANT: Cobb, Melanie  
APPLICANT: Hutchinson, Michele  
APPLICANT: Chen, Zhu  
APPLICANT: Berman, Kevin  
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26

Query Match Score 21%; DB 3; Length 190;  
Best Local Similarity 66.7%; Pred. No. 37;  
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 AGCAACATTAACAGCGTGCATTACATATTGATAATCAGGTTTC 45  
Db 8 AGAAAAACTTAAGGCCATGGCAATTAAACACTTTC 52

RESULT 5  
US-09-723-458-8  
Sequence 8, Application US/09723458  
Patent No. 6586242  
GENERAL INFORMATION:  
APPLICANT: Cobb, Melanie  
Hutchinson, Michele  
Chen, Zhu  
Berman, Kevin  
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,458  
FILING DATE: 27-No. 6586242-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,410  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.

REGISTRATION NUMBER: 31,392  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4300  
 TELEXFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 190 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear; Score 21; DB 4; Length 190;  
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 US-09-723-438-8

Query Match Score 21; DB 4; Length 190;  
 Best Local Similarity 66.7%; Pred. No. 37;  
 Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 Db 8 AGAAAACCTTAACAGCTGCAATTACTATGATAATCAGGTT 45

Qy 1 AGCAAACATTAAACAGGGTGCATTACATGATAATCAGGTT 45  
 Db 8 AGAAAACCTTAACAGCTGCAATTACTATGATAATCAGGTT 52

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RESULT 6  
 US-09-321-017B-1040/c  
 Sequence 1040, Application US/09221017B  
 ; Patent No. 6444799  
 GENERAL INFORMATION:  
 APPLICANT: ROSS, Bruce C.  
 TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
 NUMBER OF SEQUENCES: 1120  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 PAGE MILL ROAD  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSEQ for Windows Version 2.0b  
 CURRENT APPLICATION NUMBER: US/09/221,017B  
 FILING DATE: 23-DEC-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PPI1182  
 FILING DATE: 31-DEC-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PP11546  
 FILING DATE: 30-JAN-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PP2911  
 FILING DATE: 09-APR-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/AU98/01023  
 FILING DATE: 10-DEC-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Monroe, Gladys H  
 REGISTRATION NUMBER: 32,430  
 REFERENCE/DOCKET NUMBER: 27340-20021.00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-813-5600  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 1040:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 614 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular

; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: UNKNOWN  
; ORIGINAL SOURCE:  
; ORGANISM: PORPHYROMONAS GINGIVALIS  
; FEATURE:  
; NAME/KEY:  
; LOCATION: 1...614  
; US-09-221-017B-1040

Query Match Score 21; DB 4; Length 614;  
 Best Local Similarity 66.7%; Pred. No. 41;  
 Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 AGCAAACATTAAACAGGGTGCATTACATGATAATCAGGTT 45  
 Db 369 AGCAAACACTCACAGGGCAACACTTAGTGAGCATGATTTC 325

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RESULT 7  
 US-09-328-352-599/c  
 Sequence 599, Application US/09328352  
 ; Patent No. 6561958  
 GENERAL INFORMATION:  
 APPLICANT: Gary L. Breton et al.  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: GTC99-03PA  
 CURRENT APPLICATION NUMBER: US/09/328,352  
 CURRENT FILING DATE: 1999-06-04  
 NUMBER OF SEQ ID NOS: 8252  
 SEQ ID NO 599  
 LENGTH: 786  
 TYPE: DNA  
 ORGANISM: Acinetobacter baumannii  
 US-09-328-352-599

Query Match Score 21; DB 4; Length 786;  
 Best Local Similarity 73.0%; Pred. No. 42;  
 Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 8 ATTAACAGCGTGCATTACATGATAATCAGGTT 44  
 Db 341 ACTAAACAGGATCAACTACATGATAGTCAAGAT 305

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RESULT 8  
 US-09-328-352-1397/c  
 Sequence 1397, Application US/09328352  
 ; Patent No. 6561958  
 GENERAL INFORMATION:  
 APPLICANT: Gary L. Breton et al.  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: GTC99-03PA  
 CURRENT APPLICATION NUMBER: US/09/328,352  
 CURRENT FILING DATE: 1999-06-04  
 NUMBER OF SEQ ID NOS: 8252  
 SEQ ID NO 1397  
 LENGTH: 1521  
 TYPE: DNA  
 ORGANISM: Acinetobacter baumannii  
 US-09-328-352-1397

Query Match Score 21; DB 4; Length 1521;  
 Best Local Similarity 66.7%; Pred. No. 45;  
 Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 AGCAAACATTAAACAGGGTGCATTACATGATAATCAGGTT 45  
 Db 1032 AGCAAAGTATATCGGTGTAATGCGATGATTCCGACTC 988

RESULT 9  
 US-09-486-072-6/C  
 / Sequence 6, Application US/09486072  
 / Patent No. 648155  
 / GENERAL INFORMATION:  
 / TITLE OF INVENTION: GENSIS  
 / FILE REFERENCE: 111202/1  
 / CURRENT FILING DATE: 2000-05-22  
 / PRIORITY APPLICATION NUMBER: PCT/JP98/022310  
 / PRIOR FILING DATE: 1998-05-26  
 / PRIORITY APPLICATION NUMBER: JP5152624/97  
 / PRIOR FILING DATE: 1997-09-03  
 / NUMBER OF SEQ ID NOS: 30  
 / SOFTWARE: FASTSEQ for Windows Version 4.0  
 / SEQ ID NO: 6  
 / LENGTH: 2643  
 / TYPE: DNA  
 / ORGANISM: Bacteria

Query Match Score 21; DB 4; Length 2643;  
 Best Local Similarity 73.0%; Pred. No. 47;  
 Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 AGCAANACTTAACAGCGTGGATTAAATATGATAA 37  
 Db 877 ACCAACCTCAATCAGACTGCCCTAACCTAGTGTATAA 841

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RESULT 10  
 US-09-453-702B-72/C  
 / Sequence 72, Application US/09453702B  
 / Patent No. 6365723  
 / GENERAL INFORMATION:  
 / APPLICANT: Blattner, Frederick R.  
 / Burland, Valerie  
 / Perna, Nicole T.  
 / Plunkett, Guy  
 / Welch, Rod  
 / TITLE OF INVENTION: Sequences of E. coli O157  
 / NUMBER OF SEQUENCES: 265  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEES: Charles & Brady  
 / STREET: 1 South Pinckney Street  
 / CITY: Madison  
 / STATE: WI  
 / COUNTRY: US  
 / ZIP: 53701-2113  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Word Perfect 8.0  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/453,702B  
 / FILING DATE: 04-DEC-1998  
 / CLASSIFICATION: <Unknown>  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 60/110,955  
 / FILING DATE: 04-DEC-1998  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Seay, Nichols J.  
 / REGISTRATION NUMBER: 27386  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (608) 251-5000  
 / TELEFAX: (608) 251-9166  
 / INFORMATION FOR SEQ ID NO: 72:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 46819  
 / TYPE: nucleic acid

LOCATION: (1633385)..(1633385)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (191389)..(191389)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (191395)..(191395)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (231380)..(231380)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (234187)..(234187)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (234220)..(234220)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (234814)..(234814)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (309398)..(309398)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (309418)..(309418)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (312837)..(312837)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (312993)..(312993)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (319226)..(319226)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (559167)..(559167)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (559241)..(559241)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (600992)..(600992)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (622708)..(622708)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (657081)..(657081)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (657203)..(657203)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (674435)..(674435)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (682442)..(682442)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (713652)..(713652)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (741684)..(741684)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (779455)..(779455)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (855539)..(855539)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (871619)..(871619)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1084330)..(1084830)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1096846)..(1096846)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1119881)..(1119881)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1130881)..(1130881)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1310988)..(1310988)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1313224)..(1313224)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1313224)..(1313224)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1345473)..(1349473)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1345920)..(1349491)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1470091)..(1470091)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1602912)..(1602912)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1637598)..(1637598)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

LOCATION: (1664054)..(1664054)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc feature

US-08-916-421B-1

Query Match 46.2%; Score 20.8; DB 4; Length 1664976;  
 Best Local Similarity 70.0%; Pred. No. 83;  
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 5 AACATTAACAGCGTCAATTACATAATTGATAATCAGTT 44  
 Db 1077378 AAATTTAAATTCATAACAGTCATAAGTTGATATGTT 1077339

RESULT 122  
 US-09-557-884-1  
 Sequence 1, Application US/09557884  
 Patient No. 6506531  
 GENERAL INFORMATION:  
 APPLICANT: Fleischmann et al.  
 TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: MD  
 COUNTRY: USA

ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 1/2 inch diskette  
 COMPUTER: Dell Pentium  
 OPERATING SYSTEM: MS DOS v6.22  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/557,884  
 FILING DATE: 25-APR-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/476,102  
 FILING DATE: JUN-5-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Michelle S. Marks  
 REGISTRATION NUMBER: 41,971  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-309-8504  
 TELEFAX: 301-309-8439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1830121 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-557-884-1

Query Match 46.2%; Score 20.8; DB 4; Length 1830121;  
 Best Local Similarity 70.0%; Pred. No. 82;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACATTAACACCGTGAATTACATATTGATAATCGTT 44  
 Db 784657 AACGTATATCGCGCAATACACTTGAAATCAACTT 784656

RESULT 13  
 US-09-643-990A-1  
 Sequence 1 Application US/09643990A  
 Patent No. 6538289  
 GENERAL INFORMATION:  
 APPLICANT: Robert D. Fleischmann  
 Mark D. Adams  
 Owen White  
 Hamilton O. Smith  
 J. Craig Venter  
 TITLE OF INVENTION: The Nucleotide sequence of  
 the Hasmophilus influenzae Rd Genome, Fragments  
 Thereof, and Uses Thereof  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville,  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 1/2 inch diskette  
 COMPUTER: Dell Pentium  
 OPERATING SYSTEM: MS DOS v6.22  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/643,990A  
 FILING DATE: 23-AUG-2000  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/4487,429  
 FILING DATE: 1995-06-07  
 APPLICATION NUMBER: 08/426,787  
 FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:  
 NAME: Kenley K. Hoover  
 REGISTRATION NUMBER: 40,302  
 REFERENCE/DOCKET NUMBER: PB186P1C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-610-5790  
 TELEX/FAX: 310-319-8439  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1830121 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-643-990A-1

Query Match 46.2%; Score 20.8; DB 4; Length 1830121;  
 Best Local Similarity 70.0%; Pred. No. 82;  
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 5 AACATTAACACCGTGAATTACATATTGATAATCGTT 44  
 Db 784657 AACGTATATCGCGCAATACACTTGAAATCAACTT 784656

RESULT 14  
 US-09-107-532A-198/C  
 Sequence 1988, Application US/09107532A  
 Patent No. 6583255  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A. Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02354  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD-ROM IS09660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 60/085,598  
 FILING DATE: 14 May 1998  
 PRIORITY NUMBER: 60/051571  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arinello, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781)893-5007  
 TELEX/FAX: (711)893-8277  
 INFORMATION FOR SEQ ID NO: 198:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 892 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular  
 MOLECULE TYPE: DNA (Genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE: Enterococcus faecium  
 FEATURE:

NAME/KEY: misc\_feature  
 LOCATION: (B) LOCATION 1...882  
 US-09-107-332A-1988  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1988;

Query Match      45.8%; Score 20.6; DB 4; Length 882;  
 Best Local Similarity 74.3%; Pred. No. 59;  
 Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy                3 CAAACATTAACAGCGTCAATTACATATTGATAA 37  
 Db                671 CAACTATCATCAGCGTCAAATCCCTATGATAA 637

## RESULT 15

US-09-028-336-1  
 Sequence 1, Application US/09/028366  
 Patent No. 6150501  
 GENERAL INFORMATION:  
 APPLICANT: CARLOW, CLOTILDE K. S.  
 APPLICANT: HONG, XIQIANG  
 APPLICANT: MA, DONG  
 TITLE OF INVENTION: NOVEL TYROSINE-CONTAINING  
 TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: New England Biolabs, Inc.  
 STREET: 32 Tozer Road  
 CITY: Beverly  
 STATE: MA  
 COUNTRY: US  
 ZIP: 01915  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/028,366  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:

NAME: Williams, Gregory D  
 REGISTRATION NUMBER: 30301  
 REFERENCE/DOCKET NUMBER: NEB-133  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 978-927-5054  
 TELEX: 978-327-1705  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1696 base pairs

TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 25..1603  
 OTHER INFORMATION:  
 US-09-028-336-1

Query Match      45.8%; Score 20.6; DB 3; Length 1696;  
 Best Local Similarity 67.4%; Pred. No. 63;  
 Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 Qy                2 GCAACATTAACAGCGTCAATTACATATTGATAAAGGGTT 44  
 Db                528 GGAAAATTAAACATTGGCAATTTCATCATGTAAAATGGAT 570

Search completed: November 25, 2003, 12:18:16  
 Job time : 57 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 25, 2003 ; Search time 294 Seconds

Perfect score: 45 (without alignments)

Title: US-10-018-878-9

Sequence: 1 agcaacattaaacacaggctg.....acatattgtataatccggttc 45

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgcn2\_6/ptodata/1/pubpna/us07\_pubcomb.seq:\*

2: /cgcn2\_6/ptodata/1/pubpna/pct\_new\_pub.seq:\*

3: /cgcn2\_6/ptodata/1/pubpna/us06\_new\_pub.seq:\*

4: /cgcn2\_6/ptodata/1/pubpna/us05\_pubcomb.seq:\*

5: /cgcn2\_6/ptodata/1/pubpna/us04\_pub.seq:\*

6: /cgcn2\_6/ptodata/1/pubpna/pctus\_pubcomb.seq:\*

7: /cgcn2\_6/ptodata/1/pubpna/us08\_new\_pub.seq:\*

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11: /cgcn2\_6/ptodata/1/pubpna/us09c\_pubcomb.seq:\*

12: /cgcn2\_6/ptodata/1/pubpna/us09\_new\_pub.seq:\*

13: /cgcn2\_6/ptodata/1/pubpna/us10a\_pubcomb.seq:\*

14: /cgcn2\_6/ptodata/1/pubpna/us10b\_pubcomb.seq:\*

15: /cgcn2\_6/ptodata/1/pubpna/us10\_new\_pub.seq:\*

16: /cgcn2\_6/ptodata/1/pubpna/us06\_new\_pub.seq:\*

17: /cgcn2\_6/ptodata/1/pubpna/us06\_pubcomb.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	45	US-09-345-492-9	Sequence 9, Appli
c 2	23.4	52.0	200	US-09-938-842A-3804	Sequence 384, Ap
c 3	23	51.1	771	US-09-910-943-129	Sequence 129, App
c 4	23	51.1	183337	US-10-020-141-5	Sequence 5, Appli
c 5	22.6	50.2	12	US-10-032-585-6062	Sequence 602, Ap
c 6	22.4	49.8	447	US-10-027-632-338109	Sequence 238109,
7	22.4	49.8	637	US-10-027-632-238110	Sequence 238110,
8	22.4	49.8	637	US-10-027-632-238110	Sequence 238110,
9	22.4	49.8	637	US-10-027-632-238110	Sequence 238110,
10	22.4	49.8	814	US-10-027-632-148927	Sequence 148927,
11	22.4	49.8	814	US-10-027-632-148927	Sequence 148927,
12	21.8	48.4	1223	US-10-027-632-202630	Sequence 202630,
13	21.8	48.4	1223	US-10-027-632-202630	Sequence 202630,
c 14	21.8	48.4	5378	US-10-311-455-851	Sequence 1810,
c 15	21.8	48.4	1691139	US-10-057-514-1	Sequence 1, Appli
16	21.6	48.0	609	US-10-027-632-255522	Sequence 255522,

**ALIGNMENTS**

US-09-345-492-9

; Sequence 9, Application US/09345492

; GENERAL INFORMATION:

; APPLICANT: ANDERSON, DAVID A.

; INVENTOR: LIU, LIN

; PATENT NO.: US20020128457A1

; ATTORNEY: PODROVROV, SERGEY

; APPLICANT: WANG, BAOMIN

; TITLE OF INVENTION: VECTORS, CELLS AND PROCESSES FOR PYRIMIDINE NUCLEOSIDES PRODUCTION

; FILE REFERENCE: 28460/123

; CURRENT APPLICATION NUMBER: US/09/345,492

; CURRENT FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 9

; LENGTH: 45

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-345-492-9

Query Match 100.0% ; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 1.6e-06;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCAACATTAACAGCGTGCATTACATTGATAATCAGGGTC 45

Db 1 AGCAACATTAACAGCGTGCATTACATTGATAATCAGGGTC 45

RESULT 2

US-09-938-842A-3804/C

; Sequence 384, Application

; PATENT NO.: US2002016378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joe  
 APPLICANT: Wang, Xin  
 APPLICANT: Tang, Tong  
 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING SAME, AND METHODS OF USE  
 NUMBER OF SEQ ID NOS: 3  
 PRIORITY REFERENCE: CRIPI1300-3  
 CURRENT APPLICATION NUMBER: US/09/938,842A  
 CURRENT FILING DATE: 2001-08-24  
 PRIOR FILING DATE: 2000-08-24  
 PRIOR APPLICATION NUMBER: US 60/227,866  
 PRIOR FILING DATE: 2001-01-16  
 PRIOR FILING DATE: 2001-05-22  
 SEQ ID NO: 3804  
 LENGTH: 2000  
 TYPE: DNA  
 ORGANISM: Arabidopsis thaliana  
 US-09-938-842A-3-804

Query Match 52.0%; Score 23.4; DB 10; Length 2000;  
 Best Local Similarity 73.2%; Pred. No. 1.7e+02;  
 Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 3 CAAACATTAAACAGGGCAATTACATGTGATACTACGCT 43  
 Db 468 CAAGTATTATCATGTACGATTACATGTICATTAAGCT 428

RESULT 3  
 US-09-910-943-129

Sequence 129, Application US/09910943

Patent No. US20020081610A1

GENERAL INFORMATION:

APPLICANT: Hemmati-Bivanloo, Ali

APPLICANT: Altman, Curtis

TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression

FILE REFERENCE: 7529/1IG14US1

CURRENT APPLICATION NUMBER: US/09/910,943

CURRENT FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 742

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 129

LENGTH: 771

TYPE: DNA

ORGANISM: Xenopus laevis

FEATURE: misc\_feature

NAME/KEY: misc\_feature

LOCATION: (1)..(771)

OTHER INFORMATION: n may be a or g or c or t/u

US-09-910-943-129

Query Match 51.1%; Score 23; DB 9; Length 771;  
 Best Local Similarity 74.4%; Pred. No. 1.8e+02;  
 Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3 CAAACATTAAACAGGGCAATTACATGTGATACTACG 41  
 Db 435 CATACAATATACAGTGACATATATTATGGTAAATTAG 473

RESULT 4  
 US-10-020-141-5/c

Sequence 5, Application US/10020141

Publication No. US20030092013A1

GENERAL INFORMATION:

APPLICANT: McCarthy, Jeanette

APPLICANT: Ableson, Allen

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE

CURRENT APPLICATION NUMBER: US/10/020,141

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US 60/313,097  
 PRIOR FILING DATE: 2001-08-16  
 PRIOR APPLICATION NUMBER: US 60/327,485  
 PRIOR FILING DATE: 2001-10-05  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 5  
 LENGTH: 1833337  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-020-141-5

Query Match 51.1%; Score 23; DB 14; Length 1833337;  
 Best Local Similarity 74.4%; Pred. No. 7.3e+02;  
 Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 Qy 2 GCAAACTTAAACAGGGCAATTACATGTGATACTAC 40  
 Db 1323374 GCCTACATTTACTGTCTGCATAATCCTATCA 1323374

RESULT 5  
 US-10-032-585-6062/c

Sequence 6062, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:

APPLICANT: Terry, Roemer D.

APPLICANT: Bo, Jiang

APPLICANT: Charles, Boone

APPLICANT: Howard, Bussey

TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

FILE REFERENCE: 10182-005-999

CURRENT APPLICATION NUMBER: US/10/032,585

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6062

LENGTH: 447

TYPE: DNA

ORGANISM: Candida albicans

US-10-032-585-6062

Query Match 50.2%; Score 22.6; DB 12; Length 447;  
 Best Local Similarity 68.9%; Pred. No. 2.2e+02;  
 Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 AGCCAACATTAACAGGGCAATTACATGTGATACTACGGTTTC 45  
 Db 156 ACCATGATTAATATCGTTGAATCCAGTTGATAACCATTC 112

RESULT 6  
 US-10-027-632-238109

Sequence 238109, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827-129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR PUBLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SEQ ID NO: 238109  
 LENGTH: 637  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-238109

Query Match 49.8%; Score 22.4; DB 12; Length 637;  
 Best Local Similarity 72.5%; Pred. No. 2.8e+02; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 11;

Qy 4 AACATTAACAGCGTGGAAATCACATGTATAATCGGT 43  
 Db 13 AACATTACCAAGCTCCAAATTAAATTATAATGAT 52

## RESULT 7

US-10-027-632-238110  
 Sequence 238110, Application US/10027632  
 Publication No. US20030204072A9

GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632  
 CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483  
 PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/185,218  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/167,363  
 PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358  
 PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SEQ ID NO: 238110  
 LENGTH: 637  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-238110

Query Match 49.8%; Score 22.4; DB 12; Length 637;  
 Best Local Similarity 72.5%; Pred. No. 2.8e+02; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 11;

Qy 4 AACATTAACAGCGTGGAAATCACATGTATAATCGGT 43  
 Db 13 AACATTACCAAGCTCCAAATTAAATTATAATGAT 52

## RESULT 8

US-10-027-632-238109  
 Sequence 238109, Application US/10027632  
 GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.129  
 CURRENT APPLICATION NUMBER: US/10/027,632  
 PRIOR APPLICATION NUMBER: US 60/218,006  
 PRIOR FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/193,483  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/167,363  
 PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358  
 PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SEQ ID NO: 238110  
 LENGTH: 637  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-238110

Query Match 49.8%; Score 22.4; DB 12; Length 637;  
 Best Local Similarity 72.5%; Pred. No. 2.8e+02; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 11;

Qy 4 AACATTAACAGCGTGGAAATCACATGTATAATCGGT 43  
 Db 13 AACATTACCAAGCTCCAAATTAAATTATAATGAT 52

RESULT 10  
 US-10-027-632-148927

Sequence 148927, Application US/10027632  
 Publication No. US20030204075A9  
 GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632  
 CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483  
 PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/185,218  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/167,363  
 PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358  
 PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 148927  
 LENGTH: 814  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-148927

Query Match Score 49.8%; Best Local Similarity 81.2%; Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 8 ATTAACAGCGTCAATACATATTGATAATC 39  
 Db 123 AATAGAAGCCCTGCAATACATTTGAAATC 154

RESULT 11  
 US-10-027-632-148927  
 Sequence 148927, Application US/10027632  
 GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632  
 CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/167,363  
 PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358  
 PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 148927  
 LENGTH: 814  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-148927

Best Local Similarity 81.2%; Pred. No. 3e+02; Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 8 ATTAACAGCGTCAATACATATTGATAATC 39  
 Db 123 AATAGAAGCCCTGCAATACATTTGAAATC 154

RESULT 12  
 US-10-027-632-202630  
 Sequence 202630, Application US/10027632  
 GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632  
 CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/167,363  
 PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358  
 PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 148927  
 LENGTH: 814  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-148927

Query Match Score 49.8%; Best Local Similarity 70.7%; Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 4 AACATTAACAGCGTGCATTACATATTGATAATCAGGT 44  
 Db 838 ATTAATTAATGGAAATTATTTGATATTCAGGT 878

RESULT 13  
 US-10-027-632-202630  
 Sequence 202630, Application US/10027632  
 GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632  
 CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/167,363  
 PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358  
 PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 148927  
 LENGTH: 814  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-148927

Query Match Score 49.8%; Best Local Similarity 70.5%; Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SOFTWARE: FabrSEQ for Windows Version 4.0  
 SEQ ID NO 202630  
 LENGTH: 1223  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-202630

Query Match 48.4%; Score 21.8; DB 13; Length 1223;  
 Best Local Similarity 70.7%; Pred. No. 1.6e+03;  
 Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 4 AACATTAACACGGTCCAATTACATATTGATAATCGTT 44  
 Db 838 ATAATAAAATTGATGAAATTATTGATATTGATTCGGTT 878

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RESULT 14  
 US-10-311-455-1851-C  
 Sequence 1851, Application US/10311455  
 Publication No. US20030143606A1  
 GENERAL INFORMATION  
 APPLICANT: OLEK, Alexander  
 APPLICANT: PIEPENROCK, Christian  
 APPLICANT: BERLIN, Kurt  
 TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination of Invention: Cytosine methylation  
 FILE REFERENCE: 5013\_1014  
 CURRENT APPLICATION NUMBER: US/10/311,455  
 CURRENT FILING DATE: 2002-12-16  
 PRIORITY NUMBER: PCT/EP01/07537  
 PRIOR FILING DATE: 2001-07-02  
 PRIORITY NUMBER: DE 10032529.7  
 PRIOR FILING DATE: 2000-06-30  
 PRIORITY NUMBER: DE 10043826.1  
 PRIOR FILING DATE: 2000-09-01  
 NUMBER OF SEQ ID NOS: 2424  
 SEQ ID NO 1851  
 LENGTH: 5378  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE: chemically treated genomic DNA (Homo sapiens)  
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 US-10-311-455-1851

Query Match 48.4%; Score 21.8; DB 12; Length 5378;  
 Best Local Similarity 70.7%; Pred. No. 8e+02;  
 Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 4 AACATTAACACGGTCCAATTACATATTGATAATCGTT 44  
 Db 1452 AATCACTAAACTCGTACCAATAATTAAATAATT 1412

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RESULT 15  
 US-10-067-514-1/C  
 Sequence 1, Application US/10067514  
 Publication No. US2003005453A1  
 GENERAL INFORMATION  
 APPLICANT: Grettarsottir, Solveig  
 APPLICANT: Jonsdottir, Sif  
 APPLICANT: Reynisottir, Sigridur Th.  
 TITLE OF INVENTION: HUMAN STROKE GENE  
 FILE REFERENCE: 2345\_2010-003  
 CURRENT APPLICATION NUMBER: US/10/067,514  
 CURRENT FILING DATE: 2002-02-04  
 PRIORITY NUMBER: US 09/811/352  
 PRIOR FILING DATE: 2001-03-19  
 NUMBER OF SEQ ID NOS: 84  
 SOFTWARE: FabrSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 1691139

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